

## ALIGNMENTS

RESULT 1

CXAR\_MOUSE

ID CXAR\_MOUSE STANDARD; PRT; 365 AA.  
AC P97792; 009052;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Cocksackievirus and adenovirus receptor homolog precursor (mCAR).  
GN CXADR OR CAR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=97190109; PubMed=9036860;  
RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;  
RT "Isolation of a common receptor for Cocksackie B viruses and  
RT adenoviruses 2 and 5."  
RL Science 275:1320-1323 (1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H/MAI;  
RX MEDLINE=97250541; PubMed=9096397;  
RA Tomko R.P., Xu R., Philipson L.;  
RT "HCAR and MCAR: the human and mouse cellular receptors for subgroup C  
RT adenoviruses and group B coxsackieviruses."  
RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356 (1997).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA Bergelson J.M., Krithivas A., Crowell T.L., Finberg R.W.;  
RT "The murine CAR homologue (mCAR) is a receptor for coxsackie B  
RT viruses and adenoviruses."  
RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.  
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.  
CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
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CC -----  
DR EMBL; Y10320; CAA71368.1; -.  
DR EMBL; U90715; AAC53148.1; -.  
DR EMBL; Y11929; CAA72679.1; -.  
DR MGD; MGI:1201679; Cxadr.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003598; Ig\_c2.  
DR InterPro; IPR003600; Ig\_like.  
DR Pfam; PF00047; ig; 2.  
DR SMART; SM00410; IG\_like; 1.

DR SMART; SM00408; IGc2; 1.  
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;  
KW Repeat.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 365 COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR  
FT HOMOLOG.  
FT DOMAIN 20 237 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 238 258 POTENTIAL.  
FT DOMAIN 259 365 CYTOPLASMIC (POTENTIAL).  
FT DOMAIN 34 127 IG-LIKE C2-TYPE DOMAIN 1.  
FT DOMAIN 155 219 IG-LIKE C2-TYPE DOMAIN 2.  
FT DISULFID 41 120 BY SIMILARITY.  
FT DISULFID 162 212 BY SIMILARITY.  
FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 340 365 VAAPNLSRMGAVPVMIPAQSKDGSIV -> FKYAYKTDGIT  
FT VV (IN REF. 2 AND 3).  
SQ SEQUENCE 365 AA; 39947 MW; 5445B4B52A34B2A2 CRC64;

Query Match 17.6%; Score 353.5; DB 1; Length 365;  
Best Local Similarity 27.8%; Pred. No. 1.8e-16;  
Matches 113; Conservative 71; Mismatches 156; Indels 67; Gaps 15;

Qy 9 VTNLLRFLFL-GLSALAPPSRAQLQLHL PANRLQAVEGGEVVLPAWYTLHGEVSSSQPWE 67  
: || | : | : : : | : | : : : | : | : | : | :  
Db 1 MARLLCFVLLCGIADFT----SGLSITTPEQRIEKAKGETAYLPCKFTLSPE--DQGPLD 54  
Qy 68 VPFVMWFFKQKEKE--DQVLSYINGVTTSKPGVSLVY-----SMPSRNL 109  
: | : : | : : : | : : : : | : : : : : : :  
Db 55 IE---WLISPSDNQIVDQVIILYSG-----DKIYDNYYPDLKGRVHFTSNDVKSGDA 103  
Qy 110 SLRLEGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNLVPPAPPSCRLQGVPHVGAN 169  
| : : | | | | | | : | : | | | | | : | : | :  
Db 104 SINVTNLQLSDIGTYQCKVK-----KAPGVANKKFLTLVLVKPSGTRCFVDGSEEIGND 157  
Qy 170 VTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPAL-DVIRGSLSLTNLSSSMAGVYVCKAHN 228  
| :  
Db 158 FKLKCEPKESLPLQFEW-QKLSDSQTMP TPWLAEMTSPVISVKNASSEYSGTYSCTVQN 216  
Qy 229 EVGTAQCNVTLE-VSTGPGA AVVAGAVVGT LVLGLLAGLVLLYHRR---GKALEEPAND 284  
| : : | : | : : : : : : : : : : : : : : : : :  
Db 217 RVGSDQCMLRLDVVPPSNRAGTIAGAVIGTLLALVLIGAILFCCHRRKREEKYEKEVHHD 276  
Qy 285 IKEDAIAPRTLPPWKSSDTISKNGTLSSVTSARALRPPHGP RP GALTPTPSLSSQALPS 344  
| : | : : | : | : : : : : : : : : : : : : : : :  
Db 277 IRED-----VPPPKSRTSTARSYIGSNHSSL-----GSMSPSNMEGYSKTQY 318  
Qy 345 PRLPTTDGAH-PQPISSIPGGVSSSGLSRMGAVPVMVPAQSQAGSLV 390  
: : : | : : : : : : : : : : : : : : : : : :  
Db 319 NQVPSEDFERAPQSPTLAPAKVAAPNLSRMGAVPVMIPAQSKDGSIV 365

## RESULT 2

## CXAR\_HUMAN

ID CXAR\_HUMAN STANDARD; PRT; 365 AA.

AC P78310; 000694;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Cocksackievirus and adenovirus receptor precursor (Cocksackievirus B-  
DE adenovirus receptor) (hCAR) (CVB3 binding protein).

GN CXADR OR CAR.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=97190109; PubMed=9036860;

RA Bergelson J.M., Cunningham J.A., Droguett G., Kurt-Jones E.,  
RA Krithivas A., Hong J.S., Horwitz M.S., Crowell R.L., Finberg R.W.;

RT "Isolation of a common receptor for Cocksackie B viruses and  
RT adenoviruses 2 and 5.";

RL Science 275:1320-1323(1997).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=97250541; PubMed=9096397;

RA Tomko R.P., Xu R., Philipson L.;

RT "hCAR and mCAR: the human and mouse cellular receptors for subgroup C  
RT adenoviruses and group B coxsackieviruses.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:3352-3356(1997).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=20008750; PubMed=10543405;

RA Bowles K.R., Gibson J., Wu J., Shaffer L.G., Towbin J.A.,  
RA Bowles N.E.;

RT "Genomic organization and chromosomal localization of the human  
RT Cocksackievirus B-adenovirus receptor gene.";

RL Hum. Genet. 105:354-359(1999).

RN [4]

RP SEQUENCE FROM N.A.

RA Anderson C.W., Kieleczawa J., Dunn J.J., Freimuth P.;

RT "Sequence and expression of CXADR, the human gene for the  
RT coxsackievirus and adenovirus receptor.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: SERVES AS A RECEPTOR FOR GROUP B COXSACKIEVIRUSES AND  
CC SUBGROUP C OF ADENOVIRUSES (AD2 AND AD5).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.

CC -----

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CC -----

DR EMBL; Y07593; CAA68868.1; -.

DR EMBL; U90716; AAC51234.1; -.

DR EMBL; AF169366; AAF05908.1; -.

DR EMBL; AF169360; AAF05908.1; JOINED.

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DR      EMBL; AF169361; AAF05908.1; JOINED.
DR      EMBL; AF169362; AAF05908.1; JOINED.
DR      EMBL; AF169363; AAF05908.1; JOINED.
DR      EMBL; AF169364; AAF05908.1; JOINED.
DR      EMBL; AF169365; AAF05908.1; JOINED.
DR      EMBL; AF200465; AAF24344.1; -.
DR      MIM; 602621; -.
DR      InterPro; IPR003006; Ig_MHC.
DR      InterPro; IPR003598; Ig_c2.
DR      InterPro; IPR003600; Ig_like.
DR      Pfam; PF00047; ig; 2.
DR      SMART; SM00410; IG_like; 1.
DR      SMART; SM00408; IGC2; 1.
KW      Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW      Repeat.
FT      SIGNAL          1          19          POTENTIAL.
FT      CHAIN           20         365          COXSACKIEVIRUS AND ADENOVIRUS RECEPTOR.
FT      DOMAIN          20         237          EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        238         258          POTENTIAL.
FT      DOMAIN          259         365          CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          34         127          IG-LIKE C2-TYPE DOMAIN 1.
FT      DOMAIN          155        219          IG-LIKE C2-TYPE DOMAIN 2.
FT      DISULFID        41         120          BY SIMILARITY.
FT      DISULFID        162        212          BY SIMILARITY.
FT      CARBOHYD        106        106          N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD        201        201          N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE        365 AA;  40029 MW;  AB01C6346CB7FE64 CRC64;

```

Query Match 17.0%; Score 343; DB 1; Length 365;  
Best Local Similarity 27.5%; Pred. No. 9e-16;  
Matches 106; Conservative 67; Mismatches 147; Indels 66; Gaps 14;

Qy	31	LQLHL PANRLQAVEG EVVLPAWYTLHGEVSSSQPWEV FVMWFFK--QKEKEDQVLSYI	88
		:   : :     :     : :   :     :	
Db	20	LSITTPEEMIEKAKGETAYLPCKFTLSPE--DQGPLDIE--WLISPADNQKVDQVIILY	74
Qy	89	NGVTTSKPGVSLVY-----SMPSRNLSLRLEGLQEKGSGPYSCSVNVQD	132
		:   :   : :   :   :	
Db	75	SG-----DKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVK---	123
Qy	133	KQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQSPRSKPAVQYQWDRQLP	192
		:   :   :         :   :   : : :   : :     :   :	
Db	124	---KAPGVANKKIHLVVLVKPSGARC YVDGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSD	180
Qy	193	SFQTF FAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLE-VSTGPAAVVA	251
		: : : : :   :     :           :     :       : :	
Db	181	SQKMPTSWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSDQCLRLNVVPPSNKAGLIA	240
Qy	252	GAVVGTLVGLGLLAGLVLLYHRRGKALE---EPANDIKEDAIAPRTLWPWKSSDTISK	307
		: :     :   :     : :   :   :     :       : : :	
Db	241	GAIIGTLLALALI-GLIIFCCRKKRREEKYEKEVHHDIRED-----VPPPKSRTSTARS	293
Qy	308	GTLSSVTSARALRPPH--GPPRPGALTPTPSLSSQALP-SPRLPTTDGAHPQPISPIPGG	364
		: :   : :   :   :   :   :     :	
Db	294	YIGSNHSSLGSMSPSNMEGYSKT-QYNQVPSEDFERTPQSPTLP-----PAK	339
Qy	365	VSSSGLSRMGAVPVMVPAQSQAAGSLV	390
		: :           :     :       :     :	
Db	340	VAAPNLSRMGAIPVMIPAQSKDGSIV	365